

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/589,677
Source: TFWP
Date Processed by STIC: 08/28/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 08/28/2006

PATENT APPLICATION: US/10/589,677

TIME: 10:33:56

Input Set : A:\2923-769 seqlist.txt

Output Set: N:\CRF4\08282006\J589677.raw

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3 <110> APPLICANT: Onichtchouk, Daria
5 <120> TITLE OF INVENTION: Use of Secreted Protein Products for Preventing and Treating
6   Pancreatic Diseases And/Or Obesity And/Or Metabolic Syndrome
8 <130> FILE REFERENCE: 2923-769
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/589,677
C--> 10 <141> CURRENT FILING DATE: 2006-08-16
10 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/001711
11 <151> PRIOR FILING DATE: 2005-02-18
13 <150> PRIOR APPLICATION NUMBER: EP 04 003 914.1
14 <151> PRIOR FILING DATE: 2004-02-20
16 <160> NUMBER OF SEQ ID NOS: 61
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 19
22 <212> TYPE: DNA
23 <213> ORGANISM: Mus musculus
25 <400> SEQUENCE: 1
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30 <211> LENGTH: 20
31 <212> TYPE: DNA
32 <213> ORGANISM: Mus musculus
34 <400> SEQUENCE: 2
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39 <211> LENGTH: 19
40 <212> TYPE: DNA
41 <213> ORGANISM: Mus musculus
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47 <210> SEQ ID NO: 4
48 <211> LENGTH: 19
49 <212> TYPE: DNA
50 <213> ORGANISM: Mus musculus
52 <400> SEQUENCE: 4
53 gttgttcgcc atgccaaga                                     19
56 <210> SEQ ID NO: 5
57 <211> LENGTH: 22
58 <212> TYPE: DNA
59 <213> ORGANISM: Mus musculus
61 <400> SEQUENCE: 5
62 caaaagcttg tggagtcagg ct                                 22
65 <210> SEQ ID NO: 6

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66 <211> LENGTH: 31
67 <212> TYPE: DNA
68 <213> ORGANISM: Mus musculus
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74 <210> SEQ ID NO: 7
75 <211> LENGTH: 18
76 <212> TYPE: DNA
77 <213> ORGANISM: Mus musculus
79 <400> SEQUENCE: 7
80 ggtacaacct ggcggtgg 18
83 <210> SEQ ID NO: 8
84 <211> LENGTH: 23
85 <212> TYPE: DNA
86 <213> ORGANISM: Mus musculus
88 <400> SEQUENCE: 8
89 gctcacgctc atcttgctc taa 23
92 <210> SEQ ID NO: 9
93 <211> LENGTH: 18
94 <212> TYPE: DNA
95 <213> ORGANISM: Mus musculus
97 <400> SEQUENCE: 9
98 tgcccgtggc tgagccgc 18
101 <210> SEQ ID NO: 10
102 <211> LENGTH: 1285
103 <212> TYPE: DNA
104 <213> ORGANISM: Mus musculus
107 <220> FEATURE:
108 <221> NAME/KEY: CDS
109 <222> LOCATION: (514)..(1131)
110 <223> OTHER INFORMATION: SF01, cDNA: NM_026161, Protein: NP_080437
112 <400> SEQUENCE: 10
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115 agcgcggggcg accagtgtgt agcccggcgt cctcacgcag caggatagcc ggctgggacc 120
117 gaagccgacc cgcccgccac cagccaggtg ccatgctgct gctcttgctg ggcttcctag 180
119 gcccggcggc ctgctgggca ctgggcccgg ctggccctgg ctctcggag ctgcggtcag 240
121 ccttctcggc ggctcgcacc accccgctgg agggcacgtc ggagatggcg gtgaccttcg 300
123 acaaggtgta cgtgaacatc ggggggtgact tcgacgcagc caccgggagg ttccgctgtc 360
125 gcgtgccggg cgcctacttc ttctccttca cggccggcaa ggcccgcaca agagcctgtc 420
127 ggtgatgctg gtgcgcaacc gcgacgaggt gcaggcgctg gctttcgacg agcagcgacg 480
129 gccaggcgcg cggcgcgcgc cagccagagc gcc atg ctg cag ctc gac tac ggc 534
130 Met Leu Gln Leu Asp Tyr Gly
131 1 5
133 gac acg gtg tgg ctg cgg ctg cac ggc gct ccg cag tac gcg ctc ggc 582
134 Asp Thr Val Trp Leu Arg Leu His Gly Ala Pro Gln Tyr Ala Leu Gly
135 10 15 20
137 gcg ccg ggc gcc acc ttc agc ggc tac ctg gtg tac gcg gac gcc gac 630
138 Ala Pro Gly Ala Thr Phe Ser Gly Tyr Leu Val Tyr Ala Asp Ala Asp
139 25 30 35

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141 gcc gac gcg cct gcg cgc ggc ccc gcg gcc ccg gag ccg cgc tcg gcc      678
142 Ala Asp Ala Pro Ala Arg Gly Pro Ala Ala Pro Glu Pro Arg Ser Ala
143 40                               45                               50                               55
145 ttc tcc gcg gcg cgc acg cgc agc ctg gtg ggc tcg gac gcc gcc ccc      726
146 Phe Ser Ala Ala Arg Thr Arg Ser Leu Val Gly Ser Asp Ala Ala Pro
147                               60                               65                               70
149 ggc ccg cgc cac cgg ccg ttg gcc ttc gac acc gag ctg gta aac ata      774
150 Gly Pro Arg His Arg Pro Leu Ala Phe Asp Thr Glu Leu Val Asn Ile
151                               75                               80                               85
153 ggt ggc gac ttc gac gcg gcg gcc ggc gtg ttc cgc tgc cgc ctg ccg      822
154 Gly Gly Asp Phe Asp Ala Ala Ala Gly Val Phe Arg Cys Arg Leu Pro
155                               90                               95                               100
157 gga gcc tat ttc ttc tcc ttc acg ctg ggc aag ctg ccg cgc aag acg      870
158 Gly Ala Tyr Phe Phe Ser Phe Thr Leu Gly Lys Leu Pro Arg Lys Thr
159                               105                              110                              115
161 ctg tcg gtg aag ctg atg aag aac cgc gac gag gtg cag gcc atg att      918
162 Leu Ser Val Lys Leu Met Lys Asn Arg Asp Glu Val Gln Ala Met Ile
163 120                               125                               130                               135
165 tac gac gac ggc gct tcg agg cgc cgt gag atg cag agt cag agc gtg      966
166 Tyr Asp Asp Gly Ala Ser Arg Arg Arg Glu Met Gln Ser Gln Ser Val
167                               140                               145                               150
169 agg ctg ccg ctg cgg cgc ggc gac gcc gtc tgg cta ctt agc cac gat      1014
170 Arg Leu Pro Leu Arg Arg Gly Asp Ala Val Trp Leu Leu Ser His Asp
171                               155                               160                               165
173 cac gat ggc tat ggc gcc tac agc aac cac ggc aag tac atc act ttc      1062
174 His Asp Gly Tyr Gly Ala Tyr Ser Asn His Gly Lys Tyr Ile Thr Phe
175                               170                               175                               180
177 tca ggc ttc ctg gtg tac cct gac ctc gcc gcc gcc ggc ccg ccg gcc      1110
178 Ser Gly Phe Leu Val Tyr Pro Asp Leu Ala Ala Ala Gly Pro Pro Ala
179                               185                               190                               195
181 ctc aag ccc cca gag ctc tga gcctctgctt ggaggagccc gggagagccg      1161
182 Leu Lys Pro Pro Glu Leu
183 200                               205
185 tggggcatgc atgccgagcc gggaccgcgg cccgaacgcc ccaccgggtcc gagcatgact      1221
187 gcctgctcag cacgcctgga ctctgccaat aaagtggggc tgccctgtcag ccttatggtc      1281
189 ctgc                                                                    1285
192 <210> SEQ ID NO: 11
193 <211> LENGTH: 205
194 <212> TYPE: PRT
195 <213> ORGANISM: Mus musculus
197 <400> SEQUENCE: 11
199 Met Leu Gln Leu Asp Tyr Gly Asp Thr Val Trp Leu Arg Leu His Gly
200 1                               5                               10                               15
203 Ala Pro Gln Tyr Ala Leu Gly Ala Pro Gly Ala Thr Phe Ser Gly Tyr
204                               20                               25                               30
207 Leu Val Tyr Ala Asp Ala Asp Ala Asp Ala Pro Ala Arg Gly Pro Ala
208                               35                               40                               45
211 Ala Pro Glu Pro Arg Ser Ala Phe Ser Ala Ala Arg Thr Arg Ser Leu
212                               50                               55                               60

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215 Val Gly Ser Asp Ala Ala Pro Gly Pro Arg His Arg Pro Leu Ala Phe
216 65              70              75              80
219 Asp Thr Glu Leu Val Asn Ile Gly Gly Asp Phe Asp Ala Ala Ala Gly
220              85              90              95
223 Val Phe Arg Cys Arg Leu Pro Gly Ala Tyr Phe Phe Ser Phe Thr Leu
224              100             105             110
227 Gly Lys Leu Pro Arg Lys Thr Leu Ser Val Lys Leu Met Lys Asn Arg
228              115             120             125
231 Asp Glu Val Gln Ala Met Ile Tyr Asp Asp Gly Ala Ser Arg Arg Arg
232              130             135             140
235 Glu Met Gln Ser Gln Ser Val Arg Leu Pro Leu Arg Arg Gly Asp Ala
236 145              150              155              160
239 Val Trp Leu Leu Ser His Asp His Asp Gly Tyr Gly Ala Tyr Ser Asn
240              165              170              175
243 His Gly Lys Tyr Ile Thr Phe Ser Gly Phe Leu Val Tyr Pro Asp Leu
244              180              185              190
247 Ala Ala Ala Gly Pro Pro Ala Leu Lys Pro Pro Glu Leu
248              195              200              205
251 <210> SEQ ID NO: 12
252 <211> LENGTH: 1393
253 <212> TYPE: DNA
254 <213> ORGANISM: Homo sapiens
257 <220> FEATURE:
258 <221> NAME/KEY: CDS
259 <222> LOCATION: (225)..(1211)
260 <223> OTHER INFORMATION: SF01, cDNA: NM_031909, Protein: NP_114115
262 <400> SEQUENCE: 12
263 gaattcggca cgaggcgccc ggcccctggc cccagcaccc tgtccgctgc cgcctcagag      60
265 ccgggaaaag cagccggagc ccccgccgcc cctgccgcag cgcggggcgg cagcgcgcag      120
267 cccggcaccc gcagcctgca gctgcagcc cgcagcccgc agcccgagc cagatcgcg      180
269 gctcagaccg aaccgcactc gaccgcgcc cccagccagg cgcc atg ctg ccg ctt      236
270                               Met Leu Pro Leu
271                               1
273 ctg ctg ggc ctg ctg ggc cca gcg gcc tgc tgg gcc ctg ggc ccg acc      284
274 Leu Leu Gly Leu Leu Gly Pro Ala Ala Cys Trp Ala Leu Gly Pro Thr
275 5              10              15              20
277 ccc ggc ccg gga tcc tct gag ctg cgc tcg gcc ttc tcg gcg gca cgc      332
278 Pro Gly Pro Gly Ser Ser Glu Leu Arg Ser Ala Phe Ser Ala Ala Arg
279              25              30              35
281 acc acc ccc ctg gag ggc acg tcg gag atg gcg gtg acc ttc gac aag      380
282 Thr Thr Pro Leu Glu Gly Thr Ser Glu Met Ala Val Thr Phe Asp Lys
283              40              45              50
285 gtg tac gtg aac atc ggg ggc gac ttc gat gtg gcc acc ggc cag ttt      428
286 Val Tyr Val Asn Ile Gly Gly Asp Phe Asp Val Ala Thr Gly Gln Phe
287              55              60              65
289 cgc tgc cgc gtg ccc ggc gcc tac ttc ttc tcc ttc acg gct ggc aag      476
290 Arg Cys Arg Val Pro Gly Ala Tyr Phe Phe Ser Phe Thr Ala Gly Lys
291              70              75              80
293 gcc ccg cac aag agc ctg tcg gtg atg ctg gtg cga aac cgc gac gag      524

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294	Ala	Pro	His	Lys	Ser	Leu	Ser	Val	Met	Leu	Val	Arg	Asn	Arg	Asp	Glu	
295	85					90				95						100	
297	gtg	cag	gcg	ctg	gcc	ttc	gac	gag	cag	cgg	cgg	cca	ggc	gcg	cgg	cgc	572
298	Val	Gln	Ala	Leu	Ala	Phe	Asp	Glu	Gln	Arg	Arg	Pro	Gly	Ala	Arg	Arg	
299				105						110					115		
301	gca	gcc	agc	cag	agc	gcc	atg	ctg	cag	ctc	gac	tac	ggc	gac	aca	gtg	620
302	Ala	Ala	Ser	Gln	Ser	Ala	Met	Leu	Gln	Leu	Asp	Tyr	Gly	Asp	Thr	Val	
303				120					125					130			
305	tgg	ctg	cgg	ctg	cat	ggc	gcc	ccg	cac	tac	gcg	cta	ggc	gcg	ccc	ggc	668
306	Trp	Leu	Arg	Leu	His	Gly	Ala	Pro	His	Tyr	Ala	Leu	Gly	Ala	Pro	Gly	
307			135					140					145				
309	gcc	acc	ttc	agc	ggc	tac	cta	gtc	tac	gcc	gac	gcc	gac	gct	gac	gcg	716
310	Ala	Thr	Phe	Ser	Gly	Tyr	Leu	Val	Tyr	Ala	Asp	Ala	Asp	Ala	Asp	Ala	
311		150					155				160						
313	cct	gcg	cgc	ggg	ccg	ccc	gcg	ccc	ccc	gag	ccg	cgc	tcg	gcc	ttc	tcg	764
314	Pro	Ala	Arg	Gly	Pro	Pro	Ala	Pro	Pro	Glu	Pro	Arg	Ser	Ala	Phe	Ser	
315	165				170					175					180		
317	gcg	gcg	cgc	acg	cgc	agc	ttg	gtg	ggc	tcg	gac	gct	ggc	ccc	ggg	ccg	812
318	Ala	Ala	Arg	Thr	Arg	Ser	Leu	Val	Gly	Ser	Asp	Ala	Gly	Pro	Gly	Pro	
319				185					190					195			
321	cgg	cac	caa	cca	ctc	gcc	ttc	gac	acc	gag	ttc	gtc	aac	att	ggc	ggc	860
322	Arg	His	Gln	Pro	Leu	Ala	Phe	Asp	Thr	Glu	Phe	Val	Asn	Ile	Gly	Gly	
323			200						205					210			
325	gac	ttc	gac	gcg	gcg	gcc	ggc	gtg	ttc	cgc	tgc	cgt	ctg	ccc	ggc	gcc	908
326	Asp	Phe	Asp	Ala	Ala	Ala	Gly	Val	Phe	Arg	Cys	Arg	Leu	Pro	Gly	Ala	
327		215					220					225					
329	tac	ttc	ttc	tcc	ttc	acg	ctg	ggc	aag	ctg	ccg	cgt	aag	acg	ctg	tcg	956
330	Tyr	Phe	Phe	Ser	Phe	Thr	Leu	Gly	Lys	Leu	Pro	Arg	Lys	Thr	Leu	Ser	
331		230					235				240						
333	gtt	aag	ctg	atg	aag	aac	cgc	gac	gag	gtg	cag	gcc	atg	att	tac	gac	1004
334	Val	Lys	Leu	Met	Lys	Asn	Arg	Asp	Glu	Val	Gln	Ala	Met	Ile	Tyr	Asp	
335	245				250					255				260			
337	gac	ggc	gcg	tcg	cgg	cgc	cgc	gag	atg	cag	agc	cag	agc	gtg	atg	ctg	1052
338	Asp	Gly	Ala	Ser	Arg	Arg	Arg	Glu	Met	Gln	Ser	Gln	Ser	Val	Met	Leu	
339				265					270					275			
341	gcc	ctg	cgg	cgc	ggc	gac	gcc	gtc	tgg	ctg	ctc	agc	cac	gac	cac	gac	1100
342	Ala	Leu	Arg	Arg	Gly	Asp	Ala	Val	Trp	Leu	Leu	Ser	His	Asp	His	Asp	
343			280						285					290			
345	ggc	tac	ggc	gcc	tac	agc	aac	cac	ggc	aag	tac	atc	acc	ttc	tcc	ggc	1148
346	Gly	Tyr	Gly	Ala	Tyr	Ser	Asn	His	Gly	Lys	Tyr	Ile	Thr	Phe	Ser	Gly	
347		295					300					305					
349	ttc	ctg	gtg	tac	ccc	gac	ctc	gcc	ccc	gcc	gcc	ccg	ccg	ggc	ctc	ggg	1196
350	Phe	Leu	Val	Tyr	Pro	Asp	Leu	Ala	Pro	Ala	Ala	Pro	Pro	Gly	Leu	Gly	
351		310				315					320						
353	gcc	tcg	gag	cta	ctg	tgagccccgg	gccagagaag	agccccgggag	ggccagggggc								1251
354	Ala	Ser	Glu	Leu	Leu												
355	325																
357	gtgcatgccca	ggccggggccc	gaggctcgaa	agtcccgcgc	gagcgccacg	gcctccggggc											1311
359	gcgcctggac	tctgccaata	aagcggaaag	cgggcacgcg	cagcgcccgg	cagcccaggc											1371

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date